

AMENDMENTS TO THE DRAWINGS

Please replace the original Drawing Sheets showing Figures 1-18 in the present application with the attached Replacement Drawing Sheets showing Figures 1-18 with proper labeling.

Attachment: Sixty-two (62) Annotated Sheets Showing Changes

Sixty-two (62) Replacement Drawing Sheets

REMARKS

In response to the Notice to File Corrected Application Papers – Notice of Allowance Mailed (the “Notice”) dated August 4, 2009, a copy thereof is attached, Applicants hereby submit Annotated Sheets Showing Changes and Replacement Drawing Sheets containing Figures 1-18 in the present application. According to the Notice, Figures 13A, 13B, 13C, 13D, 15, 16 and 17 as originally submitted are continue over several pages without proper labeling as continuation. The Replacement Drawing Sheets containing Figures 13A, 13B, 13C, 13D, 15, 16 and 17 submitted herewith correct the aforementioned defects. Furthermore, because the total number of the drawing sheets has changed in view of the amendment made to Figure 16 in the Response dated October 24, 2007, Applicants submit herewith a complete set of the drawings that reflects the correct numbering of the Drawing Sheets. A set of Annotated Sheets Showing Changes is also enclosed to show the changes made in each drawing. In view of the present amendment, Applicants believe that the application is in compliance with 37 CFR § 1.84 and 37 CFR § 1.121(d). No new matter has been added in the Replacement Drawing Sheets submitted herewith.

This response is filed within the two-month period for response from the mailing of the Notice. No fee is believed due. However, if a fee is due, please charge our Deposit Account No. 03-2775, under Order No. 13477-00002-US from which the undersigned is authorized to draw.

Respectfully submitted,

By /s/ Hui-Ju Wu
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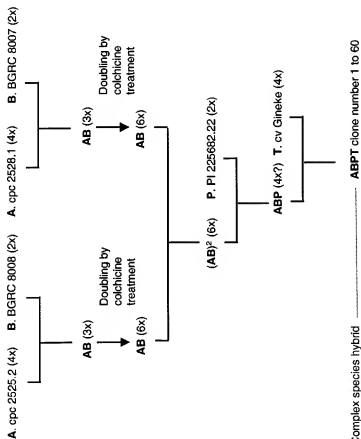


Figure 1A

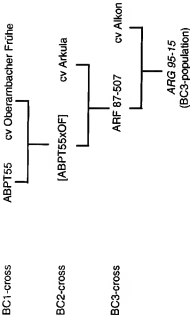


Figure 1B

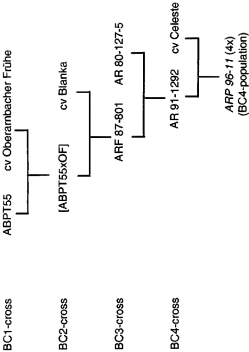


Figure 1C

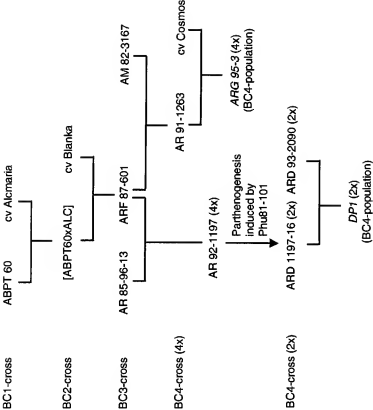
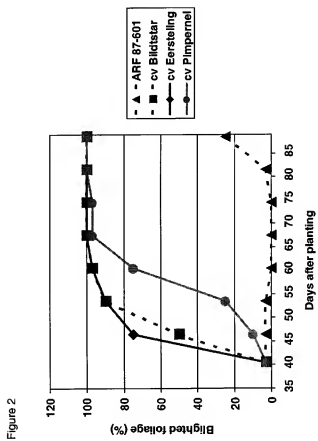


Figure 1D

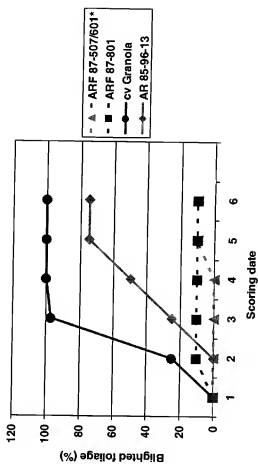
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Figure 3

* ARF 87-507 and ARF 87-601 had identical disease progress curves



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Figure 4



Figure 4 dia 3

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Figure 4 dia 4

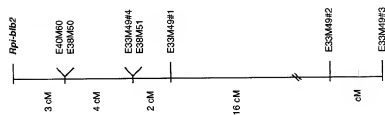
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Figure 4 dia 5



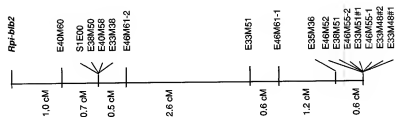
Figure 4 dia 6



ARG 95-15

Figure 5

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ARG 95-3

Figure 6

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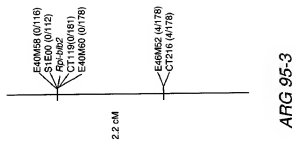


Figure 7

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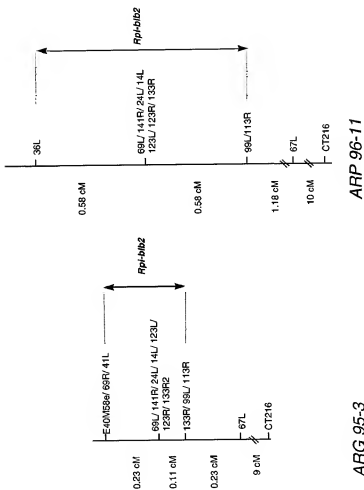
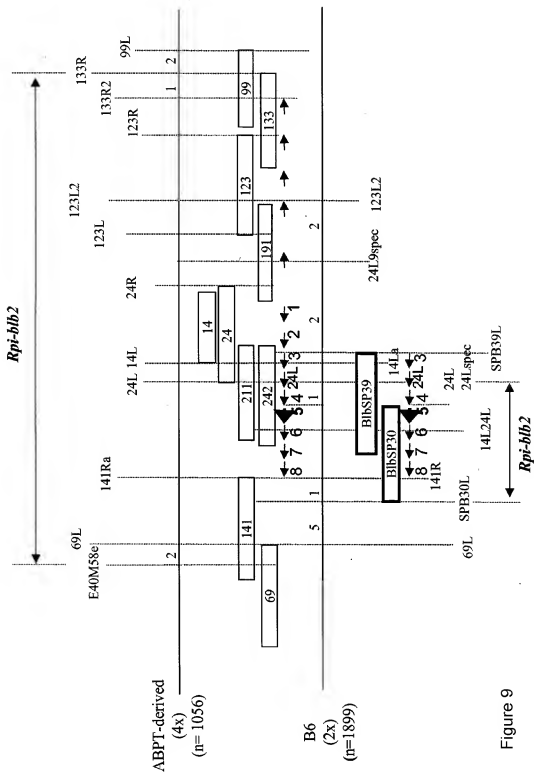


Figure 8



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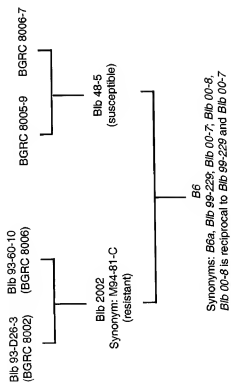


Figure 10

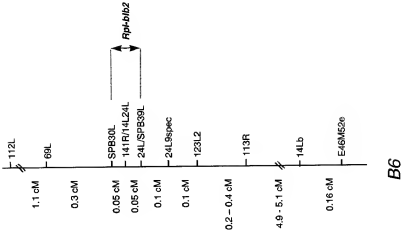


Figure 11

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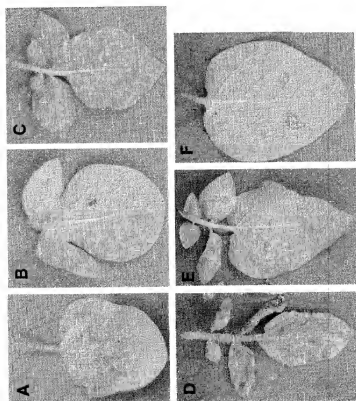


Figure 12

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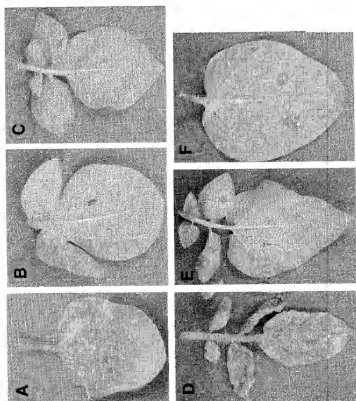


Figure 12 dia2

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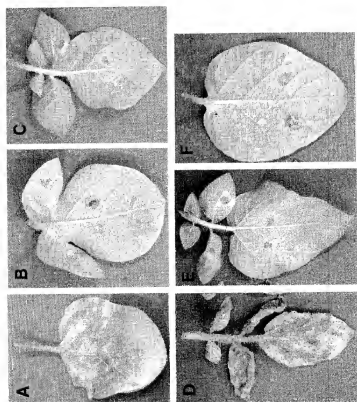


Figure 12 dia 3

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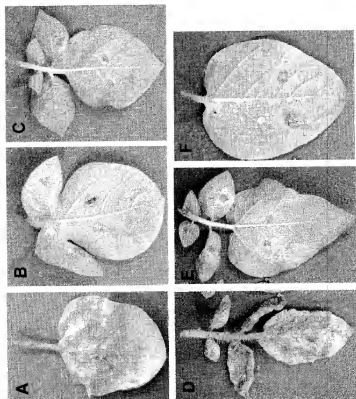


Figure 12 dia 4

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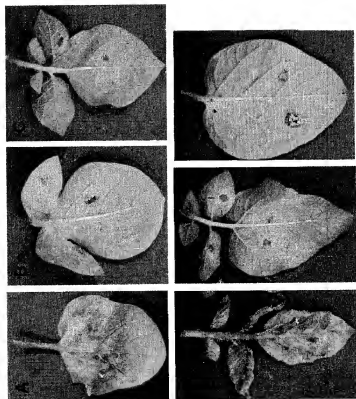


Figure 12 dia 5

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Figure 13A

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TAAAGAATGAAGAAGATCAAAAGGCTGTTGATGTGGATCTGATTGAAAGC 150
CTGAAATTGAAGCTGACATTTATTGTACATATGTCCAGCTTTCCTATTTC 200
CGATTTGGAGAAGTTTGAAGATATAATGACTAGAAAAAGACAAGAGGTTG 250
AGAATCTGCTTCAACCAATTTGGATGATGATGGCAAGACGTCGGGTGT 300
AAATATGTCCTTACTAGCTCGCCGGTAATATGGATGACTGTATAAGCTT 350
GTATCATCGTTCTAAATCAGATGCCACCATGATGGATGAGCAATGGGGCT 400
TCCTCCTCTTGAATCTCTCTCATCTATCCAAGCATCGTGCTGAAAGATG 450
TTTCCTGGAGTACTCAATATGAGGTTCTTCAGAAATGATGTGGCAACAT 500
AAGAGATTTCATGGATTGATAGTGAATTGTTGCATTAAAGCATGAGATGG 550
TTGAGAAATGCTTTATCTCTGTTTCAACTGATGGCTGAGAGAGTAGGACGC 600
TTCCTTTGGGAGGATCAGGCTGATGAAGACTCTCAACTCTCCGAGCTAGA 650
TGAGGATGATCAGAAATGATAAAGACCTCAACTCTTCAAGCTAGCACATC 700
TACTCTTGAAGATTGTTCCAACCTGAATTGGAGGTTATGCACATATGTTAT 750
AAAACTTTGAAAGCTTCAACTTCAACAGAAATTGGACGCTTCATTAAGAA 800
GCTCTGGAACCTCTCCGACATCTCAGAGAAATATCTGATTCATCTAC 850
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CAAGGACTTTATTATCATGACAAACTTTTGTATCTCTTGGCTCGTGTG 100
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GTTTTGGTGAGGAGACAACTTGATACTTAGAAAGCTCACCAGTGGACCG 1650
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Figure 13A (cont.)

GCAGATCTAGATGTCATTTTCGATCATTTGGTATGCCGGGTTTAGGTAAAC 1700
TACTTTGGCGTACAAAGTATACAATGATAAATCAGTTTCTAGCCATTTTCG 1750
ACCTTCGTGCATGGTGCACGGTCGACCAAGTATATGACGAGAAGAAGTTG 1800
TTGGATAAAATTTTCAATCAAGTTAGTGACTCAAATTCAAAATTGAGTGA 1850
GAATATTGATGTTGCTGATAAACTACGGAACAATTTGTTGGAAAGAGGT 1900
ATCTTATTGCTTAGATGACGTGTGGGATACTAATACATGGGATGAGCTA 1950
ACAAAGACCTTTTCTGATGGTATGAAAGGAAGTAGAATTATTTTGACAAC 2000
TCGAGAAAAGAAAGTTGCTTTGCATGGAAGCTCTACACTGATCCTCTTA 2050
ACCTTCGATTGCTAAGATCAGAAGAAAGTTGGGAGTTATTAGAGAAAAGG 2100
GCATTTGGAAACGAGAGTTGCCCTGATGAACATTGGATGTTGGTAAAGA 2150
AATAGCCGAAAATTGTAAAGGGCTTCCTTTGGTGGTGGATCTGATTGCTG 2200
GAATCATTGCTGGGAGGGAAAAGAAAAGAGTGTGTGGCTTGAAGTTGTA 2250
AATAATTGCAATCCTTTATTTTGAAGAATGAAGTGAAGTGATGAAAGT 2300
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TGGTAATTGTTTCAATGAGATAGGTGATTACCCTACTTGCCAACTTCAT 2550
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GCATTGATTATGATGATGATGAAGAGCACTTGGGCTTAATTTTGTCTTG 2700
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AGGACACAAAGTTAGAACTTGACAGCATTAGGGGAACCTCGTCTTTCC 3150
TATTGGAAGATACAGAGGATATTTTCAAAGGCTTCCCAATCTTCAAGT 3200
GCTTCATTTCAACTCAAGGAGTCATGGGATTATTCAACAGAGCAATATT 3250
GGTTCGCCGAAATTGGATTTCCTAAGTGAACTAGAAAACTCACTGTAGAT 3300
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GCCATGGGATTTTCACTTTCCTTCGAGTTTGAAAAGATTGCAATTGCATG 3400

Figure 13A (cont.)

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GAGAAATTAGAACTGTCGGACTGTCATAATCTTGAGGAGATTCCGCTAG 3650
TTTTGGGGATATTTATTCCTTGAAAAATTATCGAACTTGTAAAGGAGCCCTC 3700
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GGAGGGGACGAGCTTCAGATCCTTGGCCAGAAGGATATCCCGTTATTTAA 3800
GTAG 3804
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Figure 13B

ATGGAACGAAAGATAATGAAGAAGCAAACTCATGGTATGTTA 50
T TTGATAGAGTGAAGCTGAAAGTATTGAATTGTAGATATCATGTGGCTTT 100
AAAAATTTGATATGTGTTATTTTGGCAGSAGTCATTTTCTGCTCTTCGCA 150
AGGATGCTGCCAATGTTCTGGATTCTCTAGAGAGATTAAAGAAATGAAGAA 2001
GATCAAAAGGCTGTTGATGTGGATCTGATTGAAAGCCTGAAATTTGAAGCT 2501
GACATTTATTTGTACATATGTCAGCTTTCTTATTCCGATTGTGGAGAAGT 3001
TTGAAGATATAATGACTAGAAAAAGACAAGAGTTGAGAATCTGCTTCAA 3501
CCAAATTTGGATGATGATGGCAAAGACGTCGGGTGTAATATGTCCTTAC 4001
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TCAATATGAGGTTCTTCAGAATGTATGTGGCAACATAAGAGATTTCCATG 6001
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TCTCTGTTTCAACTGATGGCTGAGAGAGTAGGACGCTTCCTTTGGGAGGA 7001
TCAGGCTGATGAAGACTCTCAACTCTCCGAGCTAGATGAGGATGATCAGA 7501
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GTTCCAACCTGAATTGGAGGTTATGCACATATGTTATAAACTTTGAAAGC 8501
TTCAACTTCAACAGAAATTGGACGCTTCATTAGAAGCTCCTGGAAACCT 9010
CTCCGGACATTTCTAGAGAAATATCTGATTCACTACAAAGGCATATGATA 9510
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ACAGAGACACTTAGATGATTGCTGGATTCCAATGCTTATTCAATTGCTT 1350
TGATAAAGGAACAAATTGGGCTGGTGAAGAAGACTTGAATTTCATAAGA 1400
TCTTTTTTCGCGCAATATTGAGCAAGGATTGTATAAAGATCTCTGGGAACG 1450
TGTTCTAGATGTGGCATATGAGGCAAAAGATGTCATAGATTCAATTATTG 1500
TTCGAGATAATGGTCTCTTACATCTTATTTTCTACTTCCCATTAACAGA 1550
AAGAAGATGATGCTTATCAAAGAAGAGGCTCTGATTACATGAGAACAT 1600
TTCGAAGAACAGAGGCTCATCGTTGTGAACCTCTCCCAAGAAACAGTTG 1650

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Figure 13B (cont.)

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ACAAACTTGATACCTTAGAAAGCTCACCACTGGACCGGCAGATCTAGATGT 1750
CATTTGCATCATTGGTATGCCGGGTTTAGGTAAAACTACTTTGGCGTACA 1800
AAGTATACAATGATAAATCAGTTTCTAGCCATTTCGACCTTCGTGCATGG 1850
TGCACGGTCGACCAAGTATATACGAGAAGAAGTTGTTGGATAAAAATTTT 1900
CAATCAAGTTAGTGACTCAAATTCAAAATTGAGTGAGAATATTGATGTTG 1950
CTGATAAACTACGGAACAAATTGTTGGAAAGAGGTATCTTATTGCTCTTA 2000
GATGACGTGTGGGATACTAATACATGGGATGAGCTAACAGACCTTTTCC 2050
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TTGCTTTGCATGGAAGCTCTACACTGATCCTCTTAACCTTCGATTGCTA 2150
AGATCAGAGAAGATTGGGAGTTATTAGAGAAAAGGCAATTTGGAACGA 2200
GAGTTGCCCTGATGAATATTGGATGTTGGTAAAGAAATAGCCGAAAATT 2250
GTAAAGGGCTTCCTTTGGTGGTGGATCTGATTGCTGGAATCATTGCTGGG 2300
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CTTTATTTTGAAGAATGAAGTGGAAGTGATGAAAGTTATAGAAAATAAGTT 2400
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TCAAGGACTCATGGGATTATTCAACAGAGCAATATTGTTTCCGAAATTTG 3350
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Figure 13B (cont.)

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TCCGATTCACTATCAACAATAGCGAGACTGCTGAACCTTGAAGAGTTGTA 3550
CCTTTATCGTACAATCATCCATGGGGAAGAATGGAACATGGGAGAAGAAG 3600
ACACCTTTGAGAATCTCAAATGTTTGATGTTGAGTCAAGTGATTCCTTTCC 3650
AAGTGGGAGGTTGGAGAGGAATCTTTTCCACGCTTGAGAAATTAGAACT 3700
GTCGGA CTGTCAATAATCTTGAGGAGATTCCGTCTAGTTTTGGGGATATTT 3750
ATTCTTGAAAAATTATCGAACTTGTAAGGAGCCCTCAACTTGAAAAATTC 3800
GCTCTCAAGATTAAGGAATATGCTGAAGATATGAGGGGAGGGGACGAGCT 3850
TCAGATCCTTGGCCAGAAGGATATCCCGTTATTTAAGTAG 3890
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Figure 13C

GATCTAGAATCACCGAACCTCCCCTCGGTACAGCTCCTCCAGTTCTACCA 50
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TCTATGCTCAAAAAATCCCGAGATAAAACCCTAGATCTGCTTCAAATGCT 150
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ACTATTTTAGAAAGACTGATTGAAGGAGAAGAAGAGAGAAAAATTCATA 250
TTGAACTCATGAACCAAAATGAATGAAAAAATAATGAGAAGAACTATAC 300
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Figure 13C (cont.)

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TCGCCGGTAATATGGATGACTGTATAAGCTTGATCATCGTCTAAATCA 2000
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CTTCAACAGAAATTGGACGCTTCATTAGAAGCTCCTGGAAACCTCTCCG 2450
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CTTGATACTTAGAAAGCTCACCAGTGGACCGGCAGATCTAGATGTCAATT 3300
CGATCATTTGGTATGCCGGGTTTAGGTAAAACTACTTTGGCGTACAAAGTA 3350
TACAATGATAAATCAGTTTCTAGCCATTTTCGACCTTCGTGCATGGTGCAC 3400

Figure 13C (cont.)

GGTCGACCAAGTATATGACGAGAAGAAGTTGTTGGATAAAATTTTCAATC 3450
AAGTTAGTGACTCAAATTCAAAATTGAGTGAGAAATATTGATGTTGCTGAT 3500
AAACTACGGAACAATTGTTTGGAAAAGAGGTATCTTATTGTCTTAGATGA 3550
CGTGTGGGATACTAATACATGGGATGAGCTAACAGACCTTTTCCTGATG 3600
GTATGAAAGGAAGTAGAATTAATTTTGACAACTCGAGAAAAGAAAGTTGCT 3650
TTGCATGGAAAGCTCTACACTGATCCTCTTAACCTTCGATTGCTAAGATC 3700
AGAAAGAAAGTTGGGAGTTATTAGAGAAAAGGGCATTGGAACGAGAGTT 3750
GCCCTGATGAACTATTGGATGTTGGTAAAGAAATAGCCGAAAAATTGTAAA 3800
GGGCTTCCTTTGGTGGTGGATCGATTGCTGGAATCATTGCTGGGAGGGA 3850
AAGAAAAAGAGTGTGTGGCTTGAAGTTGTAATAAATTCATTCCTTTA 3900
TTTTGAAGATGAAGTGGAGTGATGAAAGTTATAGAAATAGTTATGAC 3950
CACTTACCTGATCACTGAAGCCATGCTTGCTGTACTTTGCAAGTGCGCC 4000
GAAGGACTGGGTAACGACAATCCATGAGTTGAAACTTATTTGGGGTTTG 4050
AAGGATTTGTGGAAGACAGATATGAAGAGTCTGGAAGAAGTGGTGAAA 4100
ATTTATTTGGATGATTTAATTTCCAGTAGCTTGGTAATTTGTTCAATGA 4150
GATAGGTGATTACCTACTTGCCTAATTCATGATCTTGTGCATGACTTTT 4200
GTTTGATAAAGCAAGAAAGGAAAAGTTGTGTGATCGGATAAGTTCAGT 4250
GCTCCATCAGATTTGTTGCCACGTCAAATTAGCATTGATTATGATGATGA 4300
TGAAGAGCACTTTGGGCTTAATTTTGCTCTGTCGGTTCAAATAAGAAAA 4350
GGCATTCCGGTAAACACCTCTATTTGACCATAAATGAGAGATGAGCTG 4400
GACGACCATCTTCTGATACATTTTCATCTAAGACACTTGAGGCTTCTTAG 4450
AACCCTTGACCTGGAATCCTCTTTTATCATGGTTAAAGATTCTTTGCTGA 4500
ATGAAATATGCATGTTGAATCATTGAGGTACTTAAGCATTGGGACAGAA 4550
GTTAAATCTCTGCCTTTGTCTTTCTCAAACCTCTGGAATCTAGAAATCTT 4600
GTTTGTGGATAACAAGAATCAACCTTGATACTATTACCGAGAATTGGG 4650
ATCTTGTAAGATTGCAAGTGCTGTTCAAGACTGCTTGTCTTTCTTTGAT 4700
ATGGATGCAGATGAATCAATACTGATAGCAGAGGACACAAAGTTAGAGAA 4750
CTTGACAGCATTAGGGGAAGCTGCTTTCTTCTATTGGAAGATACAGAGG 4800
ATATTTTCAAAGGCTTCCCAATCTTCAAGTGCTTCAATTTCAAACCTCAAG 4850
GAGTCATGGGATTATTCAACAGAGCAATATTGGTTCCCGAAATGGATTT 4900
CCTAACTGAACTAGAAAACTCACTGTAGATTTTGAAAGATCAAAACAAA 4950
ATGACAGTGGGTCTCTGACGCCATAAATCGGCCATGGGATTTTCACTTT 5000
CCTTCGAGTTTGAAAAGATTGCAATTGCATGAATTTCTCTGACATCCGA 5050
TTCCTATCAACAATAGCGAGACTGCTGAACCTTGAAAGAGTTGTACCTTT 5100
ATCGTACAATCATCCATGGGGAAGATGGAACATGGGAGAAGAGACACC 5150

Figure 13C (cont.)

TTTGAGAAATCTCAAATGTTTGATGTTGAGTCAAGTGATTCTTTCCAAGTG 5200
GGAGGTTGGAGAGGAATCTTTCCACGCTTGAGAAATTAGAACTGTCGG 5250
ACTGTCATAATCTTGAGGAGATTCCGCTAGTTTTGGGGATATTTATTC 5300
TTGAAAATTATCGAACTTGTAAGGAGCCCTCAACTTGAAAATTCGCTCT 5350
CAAGATTAAGGAATATGCTGAAGATATGAGGGGAGGGACGAGCTTCAGA 5400
TCCTTGCCAGAAAGGATATCCGTTATTTAAGTAGTTTGTGAGCATTATG 5450
GTTGAAAAGTAGATTGCACTTTGCTGGGTAGATTGATATGTTAAGAAA 5500
ATTCTGTTACAGTTGTTATGAAACATTTTTATTGACTTTTCTGAGTTTC 5550
TTTGTAGAAAACCTCAGAAGTTTTTAACAAAAATTATAGTTTTTATAAATAC 5600
AATGTGGATTGCTCTTTGGCTGTCCAACCTTGGTCTGAAGTCTCATATGCT 5650
CAGAGCACTATCGTTCACCTCAATCAAGGTACTGATTAAATGACATC 5700
TATACTACTTTATCACAAACCCAAACGAACCTTCATCTCAAAGCTAGGCC 5750
AGGAAGTGAAGAGGTTGTAGAGAGCTTATAAGCACTCATGACTTCCTTT 5800
CTCGAACATTCAACCAACGTAGGCTGAAATCCCACTCTGAACGAAAATAA 5850
GTGTTTGTTTATCAAAATAACTCTCGTAGTAGAACACTGAAATACCTTCT 5900
TCTAAACGTTCAACAAATGGGATTTCCAGCACTCAAAGTGAATGAAAGGT 5950
TCACATTAATCTTCAAAAAGAATTACGACAATTCATGACCACAAGTACAT 6000
TGACAGCACCATTCAACAGAAGAACAGTCAATGCTGCATCTTCATCAA 6050
TAATCCGAGTGTCGAACCTCCTCTCTGACACTGTCTGTATATGTAAAGT 6100
TTCTCAACAGGCAACTTTCTGGTCTCGTATCTGGATGACCCCTCTCGTC 6150
TATAACTTCAACATTAAAGCCCTGGCAACTTCTGGACCAACAGCTTACATG 6200
CTTCAAACTTACTGAACAATTAGACATCCAAAGGGATCGCATTTGTCTCC 6250
AGCTTTGCAGCATTTAGCCAACAGAGCCTCATCGCCAAAGGGGAGTCTCT 6300
AATCTCGAATTTGAAAAAATTTGTTGTTGTATGACTTTCCTCTGACATCCG 6350
ATGCACTATCAACAATAGCAAGACTGGAGTTGGAGGAGGAATCCTTTATT 6400
ATACAATCATTGAGGAGAGAAGATGGAACATGGGGGAGGAGACACTTTT 6450
GAGAATCTGAAATGTGTTAGAGCCACAAGCTACAGAAGTATTGAATTTGT 6500
CATGAATATCAACATTCTTCATCTAGTTAATTCTTTTCAATTTTTAAT 6550
AGACTCTCATTTTAACTACTAATATTCTTCTATTTGTGACTTCTTTTCTG 6600
CAGGTGGCAACTTTAAATTCAATAAGTATAGGATTGATGACAACTCGAA 6650
AAATATCTTAATGAGGTGAAGTTTGAGCAGTCAGCAGATGTTGGTTCCAA 6700
CTCTAAGTTGACAAGCACATACTATCCCGAGGGCGATTTCAGCCTGAT 6750
GCATATGTTAGTGTGGCTAGAGCAGACAGGATGTATTACCTGGATATCT 6800
ACCAAGACGAATCCACAATCAGTTTTTATGTCAAGCAATACATGAAGTAAC 6850
TCCCGATAGAACAGTAAAAGCAAGATGTGTAGGTGTATCTCGACTCTAAG 6900

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Figure 13C (cont.)

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AGATTGTACATTCCCTCTTTGAGATTTTACTGCTAATACAAATTACACC 6950
TCAGAAGCGAATCTAGAATTTCTAGAGCATGAATGCACCAC TAATGAAAG 7000
GAGAAAAAGGAAGTATGAAGTGGGAATTTGATCCTTGTTTCTAGGTATA 7050
TAAATTTTATCATTTCACTATACTTTCATTTAGCAACAACTCTCTTTGCC 7100
ATTATTTCTCAAAACAAGGGCTTCTAATATTGCTAAACTAAAGACTGTCAA 7150
AAGGTAAGTTCATCTTCAAACCTCTCTTGTTTACTTTTATCTAAAGGGGAAC 7200
TATGAAAAACAAGAAACATCAGGAATGTCCTGTAACCAAAGCAGCCTCAT 7250
GCACAAAACATCCAACGTTGGTAGGATTAATGGAGGGATCGCATCCCAGG 7300
AGGATACTGTAGAAAAATTAGTGGCTTCTTTCACCGCTCAAACCCATGAT 7350
CTATAGGTTACATGGAGACAACCTTTATGGTTGCTCGTAGGCTCCCGTCAA 7400
TTCTCATAAACCAACACCAAGTTGCATCAGACATCATCTTCATTAC 7450
AAGCTGACAATCTCCACAAGTCTTAGTCAACTTGTAAATATGAATATTAGC 7500
CAGGTAGACGTACATATTTACAAAATTGAGTTTCTATATAATATGGTTT 7550
GAAGGAATGAAACATGATGGGGAGGGTAGATAAAATAATATATGAGGCAT 7600
AAAAATAGGAAAGATATTTGTAGTGAGAGGTTTTGACTTTTTTATGCTGCT 7650
TTTGATCTTCAGTTTCTGTATTCTTTTCTACTGCTTCTCTCTCTTC 7700
TCCTGAGTAAAGTTTTATGTAGGTACTTTTATACGTCCGATCGTGAGAA 7750
CTTGAAAGAAAGCTCTCTATAGCTATGTTAGGTGCCACATAAAAAAATG 7800
AATATATCAAAAAACCTGATAATAAAATACATAATCTAAGATATTCAC 7850
TGCAACATACATGCAAAATATATATATATAAAATTTTCATGAAATATATA 7900
CAATAATAGATGTGAACATATAACTTTAAAAATAATATTACATCCATAA 7950
AGCTTAAATCTAGATC 7967
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Figure 13D

GATCTGCTTCAAATGCTCTGATACCATTGTAATTCAGTGAATTCCTAACTA 50
AACAAATGGAGAGAATTAACTATTTTAGAAAAGACTGATTGAAGGAGAAGAA 100
GAGAGAAAAATTCATATTGAACTCATGAACCAAAATGAATGAAAAAAT 150
AATGAGAAAGAACTATACCTATTACAACTATATATCTCTATTATATCTTA 200
ATCTGAAGCAGTTAATTTAACTGACTCTAAACAACCTAGACTGATAGGTGTA 250
CATTTTCTGTTAGTGCACCTGCAGTGCATTTAACCTAAGTCTTAACATAAA 300
GAATGTTGTTGCACTTCATTTCGAATAGCTTCAATGAGAAGCAAACTGT 350
GTACCTGTAAGACACACAGTAAAAGTGTAAATAATGAATAAATATGAAT 400
AAATCAAAATATAAATTAATAAATAAACAACATCCAATTAACTTTGAGG 450
TCTTGAATACTGATGGTAATTAACAAGACCCCTTGGAATTTAAGTCTG 500
TAATTGAAAAATTTGAGTATAGGTAGGGGACATTTGACTATTTTCTCATT 550
TTCTTTATCTTTTTTCTTAATTTGTGGCAGACAAGTGAGGAGGCCCACTG 600
TAATTGATTCATGCTTTTGTCTTCTTGACTTTTGGAACTACTATGCA 650
TCATATTTGGTCTTAATTTATCTCTGTTTATTTCCAGAATTTTGAGCTC 700
TATACATCTAATAACAAGCAAGCAGAGGATATATAGTTTCATCACTAA 750
AAAGGTTAGTCAACTCATCTAATATTTGCTACTCTCATCTCTATTGAAGT 800
ACAGTTATGGAAGTAGAAGTGATGTAAGAAAAATGAAAGAAGCTTTAGT 850
AGGTTAGTTGGATCTAACAAAGAGAAAGGGAATAAATTGCAGGAGAAG 900
AGAGAGGTTAAATACTTACTCACACCACCGATTTACAACAAATCACTTAA 950
TTGTGGTTAGTTAATGTATACCTTCCCTCATTTAAATTTACTTACCCA 1000
TGATAAGTTGATTAATTTGGTATTAATATCCGGTGCGGGTGAATTCCTA 1005
CCGGTGAGAGGATGGGGTTGGAGAGTGTGGAGTGAACAGAAGCAGATG 1100
TTTTAGATTTTTTCTAAGATGACGAAAGATTCCCTCTCAATGAATAATA 1150
TATTACTATACGCTATTAGAGATAGAAAGGTTCCGTACCAAGTTGGTCTCG 1200
TTTCTGGATGAACCCCATTTTTACAAGTCATTTTCTCAATTCAAATCGC 1250
AAGTGTACCTTTATCATCTTCCACTAATTAAGTCTCTTAAGTTCGCGTG 1300
AAAATAGTGAAATTTATTGATTATCTTATCATTTTCATCTTCTTCTCCTG 1350
ATAAAGTTTTATGACTTTTTATGCATCAGGCTTGAGAACTTGGAAGG 1400
AAAAGTAGAATCATGGAAAAACGAAAAAGATAATGAAGAAGCAACAACCT 1450
ATTGGTATGTTATTTGATAGAGTGAAGTGAAGTATTGAATTTGAGATA 1500
TCATGTGGCTTTAAAAATTTGATATGTGTTATTTTGGCAGGAGTCATTTT 1550
CTGCTCTTCGCAAGGATGCTGCCAATGTTCTGGATTTCCTAGAGAGATTA 1600
AAGAAATGAAGAAGATCAAAAGGCTGTTGATGTGGATCTGATGAAAGCCT 1650

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Figure 13D (cont.)

GAAATTGAAGCTGACATTTATTTGTACATATGTCCAGCTTCTTATTCGG 1700
ATTTGGAGAAGTTTGAAGATATAATGACTAGAAAAAGACAAGAGGTTGAG 1750
AATCTGCTTCAACCAATTTTGGATGATGATGGCAAAGACGTCGGGTGTAA 1800
ATATGTCCTTACTAGCCTCGCCGGTAAATATGGATGACTGTATAAGCTTGT 1850
ATCATCGTTCTAAATCAGATGCCACCATGATGGATGAGCAATTGGGCTTC 1900
CTCCTCTTGAATCTCTCATCTATCCAAGCATCGTGCTGAAAAGATGTT 1950
TCCTGGAGTGACTCAATATGAGGTTCTTCAGAATGTATGTGGCAACATAA 2000
GAGATTTCCATGGATTGATAGTGAATTGTTGCATTAAAGCATGAGATGGTT 2050
GAGAATGCTTATCTCTGTTCCTCAACTGATGGCTGAGAGAGTAGGACGCTT 2100
CCTTTGGGAGGATCAGGCTGATGAAGACTCTCAACTCTCCGAGCTAGATG 2150
AGGATGATCAGAATGATAAGACCCTCAACTCTTCAAGCTAGCACATCTA 2200
CTCTTGAAGATTGTTCCAACCTGAATTGGAGGTTATGCACATATGTTATAA 2250
AACTTTGAAAGCTTCAACTTCAACAGAAATTTGACGCTTCATTAAAGAAGC 2300
TCCTGGAAACCTCTCCGGACATCTCAGAGAATATCTGATTCACTTACAA 2350
GAGCATATGATAACTGTTATTACCCCTAACACTTCAGGGGCTCGAAACAT 2400
TCATGTCATGATGGAATTCCTATTGATTATTCTTCTGATATGCCGCCCA 2450
AGGACTTTATTTCATCATGACAAACTTTTTGATCTCTTGGCTCGTGTGTA 2500
GCACCTACCAGGAGGTATCAACTCTTGTACGCGACTTGGAGAGAAATT 2550
AAGGATTAAAGAGAGTACTGACGAAACAAATTTGCAACCCCTAAAGTTTC 2600
TGGAAAATATTGAACCTCCTTAAGGAAGATCTCAAACATGTTTATCTGAAA 2650
GTCCCGGATTCACTCAATATTGCTTCCCCTGAGTGATGGACCTCTCTTT 2700
CATGCATCTGCTACAGAGACACTTAGATGATTTGCTGGATTCCAATGCTT 2750
ATTCAATTGCTTTGATAAAGGAACAAATTTGGGCTGGTGAAGAGACTTG 2800
GAATTCATAAGATCTTTTTTCGCGAATATTGAGCAAGGATTGTATAAGA 2850
TCTCTGGGAACGTGTTCTAGATGTGGCATATGAGGCAAAAGATGTCATAG 2900
ATTCAATTATTGTTTCGAGATAATGGTCTCTTACATCTTATTTTCTCACTT 2950
CCCATTACCAGAAAGAAGATGATGCTTATCAAAGAAGAGGCTCTCTGATTT 3000
ACATGAGAACATTTCCAAGACAGAGGTCATCGTTGTGAACCTCCTCCA 3050
AGAAACACGTTGAGAGCAAGTCATTGACAACTGATAAAATAATTTAGGT 3100
TTTGGTGAGGAGACAACTTGATCTTAGAAAGCTCACCAGTGGACCGGC 3150
AGATCTAGATGTCATTTTCGATCATTGGTATGCCGGGTTTAGGTAAAACCTA 3200
CTTTGGCGTACAAAGTATACAATGATAAATCAGTTTCTAGCCATTTTCGAC 3250
CTTCGTGCATGGTGCACGGTCGACCAAGTATATGACGAGAAGAAGTTGTT 3300
GGATAAAATTTTCAATCAAGTTAGTGACTCAAATTCAAAATTTGAGTGAGA 3350
ATATTGATGTTGCTGATAAACTACGGAACCAATTGTTTGGAAAGAGGTAT 3400

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Figure 13D (cont.)

CTTATTGCTTTAGATGACGTGTGGGATACTAATACATGGGATGAGCTAAC 3450
AAGACCTTTTCCTGATGGTATGAAAGGAAGTAGAATTATTTGACAACTC 3500
GAGAAAAGAAAGTTGCTTTGCATGGAAAGCTCTACACTGATCCTCTTAAC 3550
CTTCGATTGCTAAGATCAGAGAAAGTTGGGAGTTATTAGAGAAAAGGGC 3600
ATTTGGAACGAGAGTTGCCCTGATGAACTATTGGATGTTGGTAAAGAAA 3650
TAGCCGAAAATTGTAAAGGGCTTCCTTTGGTGGTGGATCTGATTGCTGGA 3700
ATCATTGCTGGGAGGGAAAAGAAAAGAGTGTGTGGCTTGAAGTTGTAAA 3750
TAATTTGCATTCCTTTATTTTGAAGAATGAAGTGAAGTATGAAAGTTA 3800
TAGAAATTAAGTTATGACCACTTACCTGATCACCTGAAGCCATGCTTGCTG 3850
TACTTTGCAAGTGCGCCGAAGGACTGGGTAACGACAATCCATGAGTTGAA 3900
ACTTATTTGGGGTTTGAAGGATTGTGGAAAAGACAGATATGAAGAGTC 3950
TGGAGAAGTGGTGAAAATTATTTGGATGATTTAATTTCCAGTAGCTTG 4000
GTAATTTGTTTCAATGAGATAGGTGATTACCCTACTTGCCAACCTTCATGA 4050
TCTTGTGCATGACTTTTGTGTTGATAAAAGCAAGAAGGAAAAGTTGTGTG 4100
ATCGGATAAGTTCAAGTGCTCCATCAGATTTGTGTCACGTCAAATTAGC 4150
ATTGATTATGATGATGATGAAGAGCACTTTGGGCTTAATTTGTCCTGTT 4200
CGGTTCAAATAAGAAAAGGCATTCCGGTAAACACCTCTATTCTTTGACCA 4250
TAAATGGAGATGAGCTGGACGACCATCTTTCTGATACATTTCATCTAAGA 4300
CACTTGAGGCTTCTTAGAACCTTGACCTGGAATCCTCTTTATCATGGT 4350
TAAAGATTCTTTGCTGAATGAAATATGCATGTTGAATCATTTGAGGTACT 4400
TAAGCATTGGGACAGAAGTTAAATCTCGCCTTTGTCTTTCTCAAACCTC 4450
TGGAACTAGAAAATCTGTTTGTGGATAACAAAGAAATCAACCTTGATACT 4500
ATTACCGAGAATTTGGGATCTTGTAAGATTGCAAGTGCTGTCACGACTG 4550
CTTGTTCTTTCTTTGATATGGATGCAGATGAATCAATACTGATAGCAGAG 4600
GACACAAAGTTAGAGAACTTGACAGCATTAGGGGAACCTCGTGCTTTCCCTA 4650
TTGGAAAGATACAGAGGATAATTTCAAAGGCTTCCCAATCTTCAAGTGC 4700
TTCATTTCAAACCTCAAGGAGTCATGGGATTATTCAACAGAGCAATATTGG 4750
TTCCCGAAATTTGGATTTCCTAACTGAACTAGAAAACTCACTGTAGATT 4800
TGAAGATCAAAACAAATGACAGATGGGTCTCTGACGCCATAAATCGGC 4850
CATGGGATTTCCTTCCCTTCGAGTTTGAAGAAGTTGCAATTCATGAA 4900
TTTCCTCTGACATCCGATTCACTATCAACAATAGCGAGACTGCTGAACCT 4950
TGAAGAGTTGTACCTTTATCGTACAATCATCCATGGGGAAGAATGGAACA 5000
TGGGAGAAGAAGACACCTTTGAGAATCTCAAATGTTTGTATGTTGAGTCAA 5050
GTGATTCTTTCCAAGTGGGAGGTTGGAGAGGAATCTTTTCCACGCTTGA 5100
GAAATTAGAAGTGTGAGTGTGATTAATCTTGAGGAGATTCCGTCTAGTT 5150

Figure 13D (cont.)

TTGGGGATATTTATTCCTGAAAAATTATCGAACTTGTAAGGAGCCCTCAA 5200
CTTGAAAAATCCGCTCTCAAGATTAAAGGAATATGCTGAAGATATGAGGGG 5250
AGGGGACGAGCTTCAGATCCTTGCCAGAAGGATATCCCCTTATTTAAGT 5300
AGTTTTTGAGCATTATGGTTGAAAAGTAGATTGCACCTTTGCTGGGTAGAT 5350
TGATATATGGTTAAGAAAATTCTGTTACAGTTGTTATGAACATTTTTATT 5400
TGACTTTTCTGAGTTCTTTTAGAAAACCTCAGAAGTTTTTAACAAAAATT 5450
ATAGTTTTTATAAATACAATGTGGATTGCGCTTTGGCTGTCCAACTTGGT 5500
CTGAAGTCTCATATGCTCAGAGCACTATCGTTCAACCTCAATCAAGGTAC 5550
TGATTTAAAAATGACATCTATACTACTTTATCACAACCCACGAACCTTC 5600
ATCTCAAAAGCTAGGCCAGGAAGTGAAGAGGTTGTAGAGAGCTTATAAGC 5650
ACTCATGACTTCCTTTTCTCGAACATTCACCAACGTAGGCTGAAAATCCC 5700
ACTCTGAACGAAAAATAGTGTTTGTATTCAAATTAACCTCTCGTAGTAGA 5750
ACACTGAAATACCTTCTTCTAAACGTTCAACAAATGGGATTTCCAGCACT 5800
CAAAGTGAATGAAAGGTTACATTAACTCTTCAAAAGGAATTACGACAATT 5850
CATGACCACAAGTACATTGACAGCACCATTTCACAGAGAACAAGTCAA 5900
TGCTGCATCTTCATCAATAATCCGAGTGTCAACCTCCTTCTGACACTG 5950
TCCTGTATATGTAAAGTTTCTCAACAGGCAACTTTCTGGTCTCGTATCT 6000
GGATGACCCCTCTCGTCTATAACTTCAACATTAAGCCCTGGCAACTTCTG 6050
GACCAACAGCTTACATGCTTCAAACTTACTGAACAATTAGACATCCAAA 6100
GGGATCGCATTGTCTCCAGCTTTGCAGCATTAGCCAACAGAGCCTCATCG 6150
CCAAAGGGGCAGTCTCTAATCTCGAATTTGAAAAAATTGTTGTGTATGA 6200
CTTCTCTGACATCCGATGCACTATCAACAATAGCAAGACTGGAGGTTG 6250
GAGAGGAATCCTTTATTATACAATCATTCAGGGAGAAGAAATGGAACATGG 6300
GGGAGGAAGACACTTTTGAGAATCTGAAATGTGTTAGAGCCACAAGCTAC 6350
AGAAGTATGAAATTGTCATGAATATCAACATTCCTCATCCTAGTTAAAT 6400
CTTTTTCGAATTTTAAAGAGCTCTCATTTTTAATCACTAATATCTCTAT 6450
TTGTGACTTCTTTTCTGCAGGTGGCAACTTTAAATTCATAAAGTATAGGA 6500
TTGATGACAACTCGAAAAATATCTTAATGAGGTGAAGTTTGAGCAGTCA 6550
GCAGATGGTGGTTCCAACCTCTAAGTTGACAAGCACAATACATCCCGGAGG 6600
GCGATTTCAAGCCTGATGCATATGGTTAGTGTGGCTAGAGCAGACAGGAT 6650
GTATTACCTGGATATCTACCAAGACGAATCCACAATCAGTTTTTATGTCAA 6700
GCAATACATGAAGTAACCTCCGATAGAACAGTAAAAGCAAGATGTGTAGG 6750
TGTATCTCGACTTAAGAGATTGTACATTCTCTTTGAGATTTTACTGC 6800
TAATACAAATTTACACCTCAGAAGCGAATCTAGAATTTCTAGAGCATGAA 6850
TGCACCCTAATGAAAGGAGAAAAAAGGAAGTATGAAGTGGGAATTTGAT 6900

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Figure 13D (cont.)

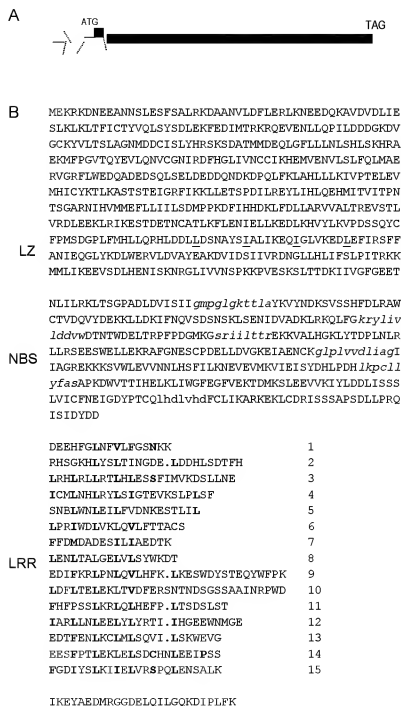
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CCTTGTTTCTAGGTATATAAAATTTATCATTCAACTATACTTCATTTAGC 6950
AAACAACTCTCTTTGCCATTATTTCTCAAACAAGGGCTCTAATATTGCT 7000
AAACTAAAGACTGTCAAAGGTAAGTTCATCTTCAAACCTCTCTGTTTAC 7050
TTTATCTAAAGGGGAACATATGAAAAACAAGAACATCAGGAATGTCCCGT 7100
AAACAAAGCAGCCTCATGACAAAAACATCCAACGTTGGTAGGATTAATGG 7150
AGGGATCGCATCCAGGAGGATACGTAGAAAAATAGTGGCTTCTTTCA 7200
CCGCTCAAACCATGATCTATAGGTTACATGGAGACAACTTTATGGTTGC 7250
TCGTAGGCTCCCGTCAATTCTCATAAACACACACCAAAGTTGCATCAG 7300
ACATCATCTTCATTCACAAGCTGACAATCTCCACAAGTCTTAGTCAACTT 7350
GTAATATGAATATTAGCCAGGTAGACGTACATATTTACAAAAATTGAGTTT 7400
CCTATATAATATGGTTTGAGGAATGAAACATGATGGGGAGGGTAGATAA 7450
AATAATATATGAGGCATAAAAAATAGGAAAGATATTTGTAGTGAGAGGTTT 7500
TGACTTTTATGCTGCTTTTGATCTTCAGTTTCTTGATTTCTTTTCTAC 7550
TGCTTTCCTCTCTTCTCCTGAGTAAAGTTTATGTAGGTACTTTTAT 7600
ACGTCGATCGTGAGAACTTGAAGAAAGCTCTCTATAGCTATGTTAGGT 7650
GCCACACATAAAAAATGAAATATTACAAAAACCTGATAATAAAATACAC 7700
TAATCTAAGATATTCAGTGCAACATACATGCAAAATATATATATATAAAT 7750
TTTCATGAAAATTATAACAAATAATAGATGTGAACATATAACTTTAAAAA 7800
TAATATTACATCCATAAAGCTTAAATTTAGATCCATCTATGCTTGTATG 7850
ATGCATAGCTCAGAATATCTCCATCAAGTGTTAACTACATATTTCAATC 7900
AAATTTATATAGAAAAACGATAATTAAGGTGAAAACTTTTATAAAGATATC 7950
GTGTGGTTGTGTGAGTGAGGTGACAAAATAAGTTGTGTGATTATTCAAAA 8000
AGTTTAAATAACGAAAATCCACATGCTTGAATTAATTGAAGCATTAAATGT 8050
TGTAACGAAAAATATTACATTTATTGAGTTACTGTGATGTTTTAACTGAT 8100
ATATAAAATAATATTGGTATTTCTCTTCATCTGCGACATAATATGTTTTT 8150
TCATCTTTTTTCAATATACAAAAATAGAATTATTATTTGTGTCATCTTT 8200
TAAGTACAAATTATTCATATGTATATAGTACAAAAATAAATATTTACTGT 8250
GGTAAAGTAAATGGAATAAGAGGTCATATTTGAAATAACAATATACTATA 8300
CTATGTTAAAGTATTTTTTATAGTTAAAATTTCTCTAGAGTACTTGATTC 8350
TACATACAAATACTAATTTCTGTAATAAATAATATTGAATTTCTTCATT 8400
GTTTCTTTATTATTAATTAGTTTATAATACTAAACTAAGGTAAATAAGA 8450
CCTTAGTTAGTTAATGTGTCTCTGTGATTTCTGTCATAGTCTAAGGG 8500
TGACTTGTGCTTATCCCAAAATGAAGGAATATCAAAAGATATATTAA 8550
AATTAAATTAATATTGTGAGGTTATGAATATAAAAGTATCAGAGTTCT 8600
ACATATAAAGAGTAACAATTGAAATAATTAAATTAATATGAGATATGAAG 8650
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Figure 13D (cont.)

GCGGACATTTAAAGAAAATAATAATAATAAAATTAAGGGTATAAAATT 8700
CATAATACATAATACCAATAAGCCGTAGAATATCTCCGTCATAATGCATA 8750
AACTAATAAATCACAAATGTATAACTCACATACAAATATTTTGTATAAA 8800
GAATTTGAATGTTGTAATAGAAATGGAGATAACTTGTGTCTTATTCCATT 8850
ATGTAAGACGTATAAATACAAATACAATGAGCTCTAATTAATTAAGGAAA 8900
CTAAATAAGGAAGGAATCAAAAAATATTATGTCATATCCCTACATATCTG 8950
CTAGAGATTCTATCATATCCTTACATATCTGTTAAGCTATGCTACACCT 9000
AAAGGTGCTACAATCATTTTGTAACTCCCTCAAGTTAGAGCATAG 9050
ATATTATTCATTCCTCAACTTGTTACAAAGATAATCAACTCGAGTTCCATT 9100
CAACGCTTTTGTGAACAAATCAACTAGTTGCTCTCCTGTCTTCACTTAGC 9150
TAGTGGATATCAGGTTTTCATGAATCTTCTACGAATAAAATGACAGTCA 9200
ACCTCAATATGTTTAGTTCTTTCATGAGACACCGGATTCAAGGCAATATG 9250
GAGCGCAACTTGATTATCATACTAGAGTTTGTATGGTATATGATGCTTCA 9300
ACCTATTTCTGTTAAAAGATAATGTATCCACATGATCTCACCATAGAC 9350
TGTAACATAACTCTGTACTTTGATTTCTGCACATAGATCAAGATACAACATT 9400
TTGCTTTTACTCTCCATGATACAGGTTTCATCCAACAAGACACAAT 9450
AACTTGATAGATCTTCTATCAATTTTCGATCCAGCCCAATCGACATCT 9500
GCAAAACACTCAATATGAGTATGGTCGTGATTTTGATACTATATTCCAAG 9550
ACTAGGAGTTTCTTCAAGTAACATAGAATATGTTCCAAAGCTGCCAGT 9600
GTTTGACGTAGGTGCAACATGAACAGCTAACAACACTTACTGCAAAAG 9650
CAATATCAAGATGAGTCACAATAAGGTAGTTTAACTTTCCAACATAACCTT 9700
TTGTATCTCTATGGATCATTAAAAGGATCGTCGTCATCTTTCATAAGATG 9750
CATATTGGGAACCATTTGGAGAACTTCAGGGTTTGCTGCCATCTTCAAT 9800
TTTCTGCAAGTAGATCGAGAGAAATATATTCTCTAAGACAAAAGAAATCCC 9850
TTTTTGTTCTATTACTTCTACTCCCAAAATGTATTCTAATTGACCCAA 9900
GTCTTTCGTATGAACCAAGTATGCAGGAAAGACTTGAGGGAAGAGATC 9949

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Figure 14



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|----------|--|------|------|------|------|------|-------|-----|-------|------|------|-----|-----|------|------|
| Mil.1 | | VL | S | I | D | V | --- | N | L | K | Q | V | K | I | MA |
| 57 | | | | | | | | | | | | | | | |
| Mil.2 | | I | VL | S | I | I | --- | N | L | K | Q | V | K | L | MA |
| 57 | | | | | | | | | | | | | | | |
| Rpi-blb2 | | MEKR | KINE | EANN | SLSP | SALR | KDAAN | WLD | FLER | LKNE | EDQK | AVD | VDL | IESL | KLKT |
| 60 | | | | | | | | | | | | | | | |
| Mil.1 | | C | F | Q | | | | L | ----- | F | TS | | | | |
| 109 | | | | | | | | | | | | | | | |
| Mil.2 | | Y | F | Q | | N | | SL | ----- | TS | | | | | |
| 109 | | | | | | | | | | | | | | | |
| Rpi-blb2 | | YV | Q | LS | Y | SD | LE | KF | E | D | I | N | T | R | K |
| 120 | | | | | | | | | | | | | | | |
| Mil.1 | | Y | I | | D | | Y | H | I | | | I | | G | |
| 169 | | | | | | | | | | | | | | | |
| Mil.2 | | Y | I | | D | | Y | H | I | | | | | L | G |
| 169 | | | | | | | | | | | | | | | |
| Rpi-blb2 | | S | - | K | S | D | A | T | M | D | E | Q | L | G | F |
| 179 | | | | | | | | | | | | | | | |
| Mil.1 | | | | P | | D | H | D | T | R | | E | R | SR | |
| 229 | | | | | | | | | | | | | | | |
| Mil.2 | | | | P | | H | T | R | | | E | H | R | SR | Q |
| 229 | | | | | | | | | | | | | | | |
| Rpi-blb2 | | R | H | E | M | V | E | N | V | L | S | L | F | Q | L |
| 239 | | | | | | | | | | | | | | | |
| Mil.1 | | V | I | T | N | | A | V | L | Q | | F | V | S | |
| 289 | | | | | | | | | | | | | | | |
| Mil.2 | | | | T | N | | A | V | | | | I | Q | L | P |
| 289 | | | | | | | | | | | | | | | |
| Rpi-blb2 | | P | T | E | L | V | M | H | I | C | Y | K | T | L | K |
| 299 | | | | | | | | | | | | | | | |
| Mil.1 | | | | L | | - | | | D | GV | | E | P | N | G |
| 348 | | | | | | | | | | | | | | | |
| Mil.2 | | | | L | | - | | | H | GT | | N | G | N | Q |
| 348 | | | | | | | | | | | | | | | |
| Rpi-blb2 | | N | I | H | V | M | E | F | L | L | I | L | S | D | M |
| 359 | | | | | | | | | | | | | | | |
| Mil.1 | | | | D | L | | K | | A | L | C | | H | I | N |
| 408 | | | | | | | | | | | | | | | |
| Mil.2 | | | | D | L | | K | | A | N | C | | H | M | N |
| 408 | | | | | | | | | | | | | | | |
| Rpi-blb2 | | T | N | C | A | T | L | K | F | L | E | N | I | E | L |
| 419 | | | | | | | | | | | | | | | |
| Mil.1 | | | | E | E | Q | K | | V | D | - | A | | A | |
| 467 | | | | | | | | | | | | | | | |
| Mil.2 | | | | S | E | E | S | Q | | G | D | A | | I | A |
| 468 | | | | | | | | | | | | | | | |
| Rpi-blb2 | | I | A | L | I | N | E | Q | I | G | L | V | K | E | D |
| 478 | | | | | | | | | | | | | | | |
| Mil.1 | | | | I | I | X | | I | A | D | P | D | | R | T |
| 527 | | | | | | | | | | | | | | | |
| Mil.2 | | | | I | I | X | | I | A | D | P | D | | R | I |
| 528 | | | | | | | | | | | | | | | |
| Rpi-blb2 | | H | L | I | F | S | L | P | I | T | A | K | K | M | L |
| 538 | | | | | | | | | | | | | | | |
| Mil.1 | | | | S | | T | S | | | | | | R | | G |
| 538 | | | | | | | | | | | | | | | |

FIGURE.15

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| | | | | | | | | |
|----------|--|-------|-----|-----|------|------|----|------|
| M11.2 | | T | S | | R | | G | D |
| 588 | | | | | | | | |
| Rpi-blb2 | TNLIIRKLITSGPADLDVISIlgmpglgkctlaYKVYNDKSVSSHFDLRANCTVDGVDEK | | | | | | | |
| 598 | | | | | | | | |
| M11.1 | NT | S | D | | | T | | ESK |
| 647 | | | | | | | | |
| M11.2 | T | S | G | D | N | | T | L |
| 648 | | | | | | | | EAK |
| Rpi-blb2 | KLIDKIFRQVSDSNKLSLENIDVADKLIRQLFGKryliivddvdtWTMDLTRFPDGM | | | | | | | |
| 658 | | | | | | | | |
| M11.1 | | E | N | D | PD | | | |
| 707 | | | | | | | | |
| M11.2 | | E | N | D | PD | D | T | |
| 708 | | | | | | | | |
| Rpi-blb2 | KGSRIILTREKKVALHGKLYTDPLMLRLLRSEESWELLEKRAFGNESCPDELLDVGEI | | | | | | | |
| 718 | | | | | | | | |
| M11.1 | | A | V | R | QSS | S | NS | L |
| 767 | | | | | | | | H |
| M11.2 | | A | V | R | QSS | S | NS | L |
| 768 | | | | | | | | H |
| Rpi-blb2 | AENCKgIplvvdliagIAGREKKKSVWLEVYVNLBSFILKNEVEVMKVEISYDHLFDH | | | | | | | |
| 778 | | | | | | | | |
| M11.1 | | F | TSL | Y | NUVF | A | G | EN |
| 827 | | | | | | | | M |
| M11.2 | | H | W | TPL | YLF | TVYL | A | E |
| 828 | | | | | | | | GI |
| Rpi-blb2 | lkpcillyfasAPKDWVTTHLKLINGFEGFVEXTDNKSLSEEVVKIYDDLISSSLVICF | | | | | | | |
| 838 | | | | | | | | |
| M11.1 | | YALNF | I | | N | F | Q | R |
| 886 | | | | | | | | T |
| M11.2 | | ILNF | I | | N | F | R | |
| 888 | | | | | | | | T |
| Rpi-blb2 | NEIGDYPTCQIhdvhdFCLIKARRENLCDRISSAPSDLLFRQISIDYDDDEEHFGLNF | | | | | | | |
| 898 | | | | | | | | IRR |
| M11.1 | | M | D | | R | I | Q | SV |
| 946 | | | | | | | | A |
| M11.2 | | M | D | | R | Q | SV | A |
| 948 | | | | | | | | I |
| Rpi-blb2 | VLEGSNKVXHSCKHLYSLTINGDELDDMLSDTFHLRHLRLRLTWHLSESEIMVKDSLNE | | | | | | | |
| 958 | | | | | | | | |
| M11.1 | | | | | | | | |
| 1006 | | | D | Q | Y | | S | STNR |
| M11.2 | | | R | R | Q | Y | F | S |
| 1008 | | | | | | | | S |
| Rpi-blb2 | ICMLNHLRYISLGVYKSLPLSPSNLANLELTVNKESTLILLPRIMDLVKLQVYVTTA | | | | | | | |
| 1018 | | | | | | | | |
| M11.1 | | | | | | | | |
| 1056 | | | | | | | | |
| M11.2 | | | | | | | | |
| 1068 | | | | | | | | |
| Rpi-blb2 | CSPFDDMADESILIAETDKLENLTAIGELVLSYWDTEIDFKRIENQLVHFKLPESWDY | | | | | | | |
| 1078 | | | | | | | | |
| M11.1 | | | | | | | | |
| 1126 | | | | | | | | |
| M11.2 | | | | | | | | |
| 1128 | | | | | | | | |

FIGURE 15 (cont.)

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| | | | | | | | | | | | | | | | |
|----------|---|---|----|----|---|--|--|--|--|---|------|----|---|------|----|
| Rpi-b1b2 | STEQTWFPKLDFLTELEKLTVDVPRSRNTNDSGSSAAINRFWDFHFPSSLKRLQLMEEP | | | | | | | | | | 11 | | | | |
| 1138 | | | | | | | | | | | | | | | |
| M11.1 | P | S | H | | | | | | | F | NFN | SI | | | |
| 1186 | | | | | | | | | | | | | | | |
| M11.2 | P | N | S | D | Q | | | | | | | F | N | RLLT | |
| 1188 | | | | | | | | | | | | | | | |
| Rpi-b1b2 | SDSLSTIARLLNLLELYLVETIINGEENMGEDTFENLKQIMLSQVLSKWEVGESFP | | | | | | | | | | | | | | |
| 1198 | | | | | | | | | | | | | | | |
| M11.1 | N | K | RG | K | P | | | | | S | KI | K | D | 13 | |
| 1246 | | | | | | | | | | | | | | | |
| M11.2 | N | K | QE | GK | P | | | | | P | KI | K | D | K | ND |
| 1248 | | | | | | | | | | | | | | | |
| Rpi-b1b2 | TLEKLELSDCHNLEEIPSGDIYSLKILVLRSPQLNSALXIKIYAEDMRGGDELQIL | | | | | | | | | | | | | | |
| 1258 | | | | | | | | | | | | | | | |
| M11.1 | N | | | | | | | | | | | | | 14 | |
| 1255 | | | | | | | | | | | | | | | |
| M11.2 | N | | | | | | | | | | | | | 15 | |
| 1257 | | | | | | | | | | | | | | | |
| Rpi-b1b2 | GQKDIPLFK | | | | | | | | | | 1267 | | | | |

FIGURE 15 (cont.)

Figure 16: Multiple Sequence Alignments of Mil.1, Mil.2 and Rpi-blb2 nucleic acids

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CLUSTAL W (1.82) Multiple Sequence Alignments

Sequence format is Pearson
Sequence 1: Mil.1          3768 bp
Sequence 2: Mil.2          3774 bp
Sequence 3: Rpi-blb2       3804 bp
Start of Pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score: 95
Sequences (1:3) Aligned. Score: 89
Sequences (2:3) Aligned. Score: 89
Guide tree      file created: [/ebi/extern/clusterw-
work/interactive/clusterw-20040503-14435620.dnd]
Start of Multiple Alignment
There are 2 groups
Aligning...
Group 1: Sequences: 2      Score:68908
Group 2: Sequences: 3      Score:65855
Alignment Score 66872
CLUSTAL-Alignment file created [/ebi/extern/clusterw-work/interactive/clusterw-
20040503-14435620.aln]

CLUSTAL W (1.82) multiple sequence alignment

Mil.1      ATGGAACGAAAGATATGAAGCAACCAACTCATGGTGGTATTTTCGCTCTT 60
Mil.2      ATGGAACGAAAGATATGAAGCAACCAACTCATGGTGGTATTTTCGCTCTT 60
Rpi-blb2   ATGGAACGAAAGATATGAAGCAACCAACTCATGGTGGTATTTTCGCTCTT 60
*****

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Figure 16 (cont.)

| | |
|----------|---|
| M1.1.1 | ACCAAGGACATTCGCGATGTTCTGGTTTTCCTTAGAGA-----ATGAGGAAATCAA 111 |
| M1.1.2 | ACCAAGGACATTCGCGATGTTCTTAATTTTCCTTAGAGA-----ATGAGGAAATCAA 111 |
| Rpl-b1b2 | CGCAAGGANTCGCCCAATGTTCTGGAATTCCTTAGAGGATTAAGAATGAGAAGATCAA 120 |
| | ***** ** |
| M1.1.1 | AAAGCTCTTGACAAAGATCAAGTTGAAAAGATAAAATGAAAATGGCAATTTATTGTACA 171 |
| M1.1.2 | AAAGCTCTTGACAAAGATCAAGTTGAAAAGCTAAAATGAAAATGGCAATTTATTGTACA 171 |
| Rpl-b1b2 | AAGGCTGTTGATGTGATCTGATTGAAAGCCTGAAATGGAAGCTGCACATTTATTGTACA 180 |
| | ** *** ** |
| M1.1.1 | TATGTTCAAGCTTTCCTGATTTTGACGAGTTTGAAGATATAATGACTAGAAAAGA 231 |
| M1.1.2 | TATGTTCAAGCTTTCCTGATTTTGACGAGTTTGAAGATATAATGACTAGAAAAGA 231 |
| Rpl-b1b2 | TATGTCAGCTTTCCTGATTTTGACGAGTTTGAAGATATAATGACTAGAAAAGA 240 |
| | ***** ** |
| M1.1.1 | CAAGAGGTTGAGAATCTGTTCAACCACTTTTGGATGATGATG----- 274 |
| M1.1.2 | CAAGAGGTTGAGAATCTGTTCAACCACTTTTGGATGATGATG----- 274 |
| Rpl-b1b2 | CAAGAGGTTGAGAATCTGTTCAACCACTTTTGGATGATGATGCGCAAGACGTCGGGTGT 300 |
| | ***** ** |
| M1.1.1 | -----TCTTTACTAGCCTCACCAGTAATGAGTACTGTATCAGCTTGTATCATCGT 327 |
| M1.1.2 | -----TCTTTACTAGCCTCACCAGTAATGAGTACTGTATCAGCTTGTATCATCGT 327 |
| Rpl-b1b2 | AAATATGTCCTTACTAGCCTCAGCGGTAAATGAGTACTGTATTAAGCTTGTATCATCGT 360 |
| | ** ***** ** |
| M1.1.1 | TCTTATAATCAGATGCCATCATGATGATGAGCAATGAGACTTCCTCCTCTTGAATCTC 387 |
| M1.1.2 | TCTTATAATCAGATGCCATCATGATGATGAGCAATGAGACTTCCTCCTCTTGAATCTC 387 |
| Rpl-b1b2 | TCTT-----AAATCAGATGCCATCATGATGATGAGCAATGAGGTTCTCCTCCTTGAATCTC 417 |
| | *** ***** ** |

Figure 16 (cont.)

| | | |
|----------|---|-----|
| M1.1.1 | TATCATCTATCCAAAGCATCACGCTGAAAAGATATTTCTCGAGTGACTCAATATGAAGTT | 447 |
| M1.1.2 | TATCATCTATCCAAAGCATCACGCTGAAAAGATATTTCTCGAGTGACTCAATATGAAGTT | 447 |
| Rpl-b1b2 | TCTCATCTATCCAAAGCATCTGCTGAAAAGATGTTTCTCGAGTGACTCAATATGAAGTT | 477 |
| | * **** | |
| M1.1.1 | CTTCAGAAATATGTGCGAACATAAAGAGATTTCCATGGGTTGATAGTGAATGGTTGCATT | 507 |
| M1.1.2 | CTTCAGAAATATGTGCGAACATAAAGAGATTTCCATGGGTTGATAGTGAATGGTTGCATT | 507 |
| Rpl-b1b2 | CTTCAGAAATGTATGTGCGAACATAAAGAGATTTCCATGGATTTGATAGTGAATGGTTGCATT | 537 |
| | ***** | |
| M1.1.1 | AAGCATGAGATGGTTGAGAAATGCTTTCCTCTGTTTCAACTCATGCGCTGACAGAGTAGGA | 567 |
| M1.1.2 | AAGCATGAGATGGTTGAGAAATGCTTTCCTCTGTTTCAACTCATGCGCTGAGAGAGTAGGA | 567 |
| Rpl-b1b2 | AAGCATGAGATGGTTGAGAAATGCTTTCCTCTGTTTCAACTCATGCGCTGAGAGAGTAGGA | 597 |
| | ***** | |
| M1.1.1 | CAGTTCCTTTGGGATGATCAGACTGATGAAGACTCTCGACTCTCCGAGCTAGATGAGGAT | 627 |
| M1.1.2 | CAGTTCCTTTGGGAGGATCAGACTGATGAAGACTCTCGGCTCTCCGAGCTAGATGAGGAT | 627 |
| Rpl-b1b2 | CGGTTCTTTGGGAGGATCAGGCTGATGAAGACTCTCAACTCTCCGAGCTAGATGAGGAT | 657 |
| | * **** | |
| M1.1.1 | GAACAAATGATAGAGACTCTCGACTTTTTCAGCTAGACATCTACTCTTTGAAGATCGTT | 687 |
| M1.1.2 | GAACAAATGATAGAGACTCTCGACTTTTTCAGCTAGACATCTACTCTTTGAAGATCGTT | 687 |
| Rpl-b1b2 | GATCAGAAATGATAAAGACCTCAACTCTTCCAGCTAGACATCTACTCTTTGAAGATCGTT | 717 |
| | ** ** | |
| M1.1.1 | CGGTTGACTCGAGGTTATACACATATGTTATACAACTTGAAGCTTCACTTCAGCT | 747 |
| M1.1.2 | CGAACTGAATGGAGGTTATGCACATATGTTATACAAATTTGAAGCTTCACTTCAGCT | 747 |
| Rpl-b1b2 | CGAACTGAATGGAGGTTATGCACATATGTTATACAAATTTGAAGCTTCACTTCAGCT | 777 |
| | ** **** | |
| M1.1.1 | GAAGTTGACTCTTTCATTAGCAGCTTCTAGAAACCTCTCCAGATATTCGTGAGGGAATAT | 807 |

Figure 16 (cont.)

| | | |
|----------|--|------|
| M1.1.2 | GAAGTTGGAGCGCTTCATTAAAGAGCTCTCGAAACCTCACCGGATATTCTCAGAGATAT | 807 |
| Rp1-b1b2 | GAATTTGGAGCGCTTCATTAAAGAGCTCTCGAAACCTCACCGGATATTCTCAGAGATAT | 837 |
| | *** ***** | |
| M1.1.1 | CTAATTCCTCTGAAGAGCAGATGGTAACTCTGTTATACCCCTAGCACTTCAGGGGCTCGA | 867 |
| M1.1.2 | ATCATTCACATCAAGAGCATATGTTAACTGTTATTCCTCCCTAGCACTTTAGGGGCTCGA | 867 |
| Rp1-b1b2 | CTGATTCATCTCAAGAGCATATGATTAACCTGTTATACCCCTAGCACTTCAGGGGCTCGA | 897 |
| | * **** ** ***** | |
| M1.1.1 | AACATTCATGTCATGATGGAAATTCCTATTACTTATCTTCTGATATGCC---CAGGGAC | 924 |
| M1.1.2 | AACATTCATGTCATGATGGAAATTCCTATTACTTATCTTCTGATATGCC---CAGGGAC | 924 |
| Rp1-b1b2 | AACATTCATGTCATGATGGAAATTCCTATTGATTAATCTTCTGATATGCCGCCCAAGGAC | 957 |
| | ***** | |
| M1.1.1 | TTTATTTCATCATGACAAACTTTTTTGATCTCTTGGATCGTCTGGAGTACTTTACAGGGAG | 984 |
| M1.1.2 | TTTATTTCATCATGACAAACTTTTTTGATCTCTTGGATCATGTTGGAACACTTTACAGGGAG | 984 |
| Rp1-b1b2 | TTTATTTCATCATGACAAACTTTTTTGATCTCTTGGATCTGCTGGTGTAGCACTTTACAGGGAG | 1017 |
| | ***** | |
| M1.1.1 | GTATCAACTCTTGTCAGTCTTGAAGAGGAACCAAGGAAATAAAGAGGGTAAATACCAA | 1044 |
| M1.1.2 | GTATCGACTCTTGTCAGTCTTGAAGAGGAATTTAAGGAAATAAAGAGGGTAAATACCAA | 1044 |
| Rp1-b1b2 | GTATCAACTCTTGTCAGTCTTGAAGAGGAATTTAAGGATTAAGAGAGTACTTGACGAA | 1077 |
| | ***** | |
| M1.1.1 | ACAAATTTGCGAACCCTAGACTTGTCTGGAATATTTGAACCTCTCAGAAAGATCTCAA | 1104 |
| M1.1.2 | ACAAATTTGCGAACCCTAGACTTGTCTGGAATATTTGAACCTCTCAGAAAGATCTCAA | 1104 |
| Rp1-b1b2 | ACAAATTTGCGAACCCTAAGTTTCTGGAATATTTGAACCTCTCTTAAGGAAGATCTCAA | 1137 |
| | ***** | |
| M1.1.1 | CATGTTTATCTGAAGCCCTGGATTCATCTCAATGTTGTTCCCATGATGATGGACCA | 1164 |
| M1.1.2 | CATGTTTATCTGAAGCCCAATTCATCTCAATGTTGTTCCCATGATGATGGACCA | 1164 |

Figure 16 (cont.)

| | |
|----------|---|
| Rpl-b1b2 | CATGTTTATCTGAAGTCCGGATTCAATCTCAATATTGCTTCCCATGAGTGATGCACCT 1197 ***** ** ***** |
| M1.1.1 | CTCTTCATGCATCTTCACACATACACTTAATAGATTGTGTAGATCTCTATGCTTTATCA 1224 |
| M1.1.2 | CTCTTCATGCATCTTCACACATGACTTAATAGATTGTGTAGATCTCTATGCTTTATCA 1224 |
| Rpl-b1b2 | CTCTTCATGCATCTTCACACATGACTTAGATGATTGTGTGATCTCAATGCTTTATCA 1257 ***** * ***** |
| M1.1.1 | ATTGCTTTGTATAAGGAAGAATCGAGCTGGTGAAGCAAGACCTGAAATTCATAAGATCA 1284 |
| M1.1.2 | ATTCTTTGTATAAGGAAGAATCGAGTTGGTGAAGCAAGACCTGAAATTCATAAGATCA 1284 |
| Rpl-b1b2 | ATTGCTTTGTATAAGGAAGAATCGAGCTGGTGAAGCAAGACCTGGAATTCATAGATCT 1317 *** ***** |
| M1.1.1 | TTCTTTGTGGATGCTG---AGCAAGGATTTGTATAAGATCTCTGGGCACTGTTCTAGAT 1341 |
| M1.1.2 | TTCTTTGGGATGCTGCTGTGACGACGATTTGTATAAGATCTCTGGGCACTGTTCTAGAT 1344 |
| Rpl-b1b2 | TTTTTCGCAATATTG---AGCAAGGATTTGTATAAGATCTCTGGGCACTGTTCTAGAT 1374 ** ** * ** ***** |
| M1.1.1 | GTGGCTTATGAGGCAAAAGATGTCATAGATTCATTTATTGTTTCGAGATATGGTCTCTTA 1401 |
| M1.1.2 | GTGGCTTATGAGGCAAAAGATGTCATAGATTCATTTATTGTTTCGAGATATGGTCTCTTA 1404 |
| Rpl-b1b2 | GTGGCATATGAGGCAAAAGATGTCATAGATTCATTTATTGTTTCGAGATATGGTCTCTTA 1434 ***** |
| M1.1.1 | CATCTTTATTTCTCATTCCATTACCATTAAGAGATCAACCTTATCAAGAGAGATC 1461 |
| M1.1.2 | CATCTTTATTTCTCATTCCCATTAAGAGATCAACCTTATCAAGAGAGATC 1464 |
| Rpl-b1b2 | CATCTTTATTTCTCATTCCCATTAAGAGATGATGATGCTTTATCAAGAGAGGTC 1494 ***** |
| M1.1.1 | TCCTGTTTATGATGAGACATTTCCCAAGGACAGAGGCTTAATCGTTGTGAACCTCCCAAG 1521 |
| M1.1.2 | TCCTGTTTATGATGAGACATTTCCCAAGGACAGAGGCTTAATCGTTGTGAACCTCCCAAG 1524 |
| Rpl-b1b2 | TCGTGATTTACATGAGACATTTCCCAAGGACAGAGGCTCATCGTTGTGAACCTCCCAAG 1554 |

Figure 16 (cont.)

| | | |
|----------|---|-----------------|
| M1.1.1 | GATGACGTGTGGGATACTACATGGGATGAGTTAAACAAGACCTTTTCTCGAATCTAAG | 1941 |
| M1.1.2 | GATGATGTGTGGGATACTACTCATTTGATGAGTTGCAAGACCTTTTCTCGAAGCTAAG | 1944 |
| Rp1-blb2 | GATGACGTGTGGGATACTATATACATGGGATGAGCTAACAGACCTTTTCTCGATGCTATG | 1974 |
| | **** * * * * * | **** * * * |
| M1.1.1 | AAAGGAGTAGGATTAATTTTGACAACTCGGGAAAAGAGTGGCTTTGCGATGGAAAAGCTG | 2001 |
| M1.1.2 | AAAGGAGTAGGATTAATTTTGACAACTCGGAAAAGGAGTGGCTTTGCGATGGAAAAGCTG | 2004 |
| Rp1-blb2 | AAAGGAGTAGAATTAATTTTGACAACTCGGAAAAGGAGTGGCTTTGCGATGGAAAAGCTC | 2034 |
| | ***** * * * * * | ***** * * * * * |
| M1.1.1 | AACACTGATCCTCTTGACCTTCGATTGCTAAGCACCAGATGAAAGTTGGGAACTATTAGAG | 2061 |
| M1.1.2 | AACACTGATCCTCTTGACCTTCGATTGCTAAGCACCAGATGAAAGTTGGGAACTTTTAGAT | 2064 |
| Rp1-blb2 | TACACTGATCCTCTTAACCTTCGATTGCTAAGATCAGAAAGTTGGGAGTTATTAGAG | 2094 |
| | ***** * * * * * | ***** * * * * * |
| M1.1.1 | AAAAGGCAATTTGGGAATGAGAGTTGCCCTGATGAACCTATTAGATGTCGGTAAAGAAATA | 2121 |
| M1.1.2 | AAAAGGCAATTTGGGAATGAGAGTTGCCCTGATGAACCTATTAGATGTCGGTAAAGAAATA | 2124 |
| Rp1-blb2 | AAAAGGCAATTTGGGAACGAGAGTTGCCCTGATGAACCTATTAGATGTCGGTAAAGAAATA | 2154 |
| | ***** * * * * * | ***** * * * * * |
| M1.1.1 | GCGGAAAATTTGTAAGGGCTTCCTTTGGTGGCTGATCTGATTCGTGGAGTCATTCGTGGG | 2181 |
| M1.1.2 | GCGGAAAATTTGTAAGGGCTTCCTTTGGTGGCTGATCTGATTCGTGGAGTCATTCGTGGG | 2184 |
| Rp1-blb2 | GCGGAAAATTTGTAAGGGCTTCCTTTGGTGGCTGATCTGATTCGTGGAGTCATTCGTGGG | 2214 |
| | ***** * * * * * | ***** * * * * * |
| M1.1.1 | AGGGAAGAAAGAGAGTGTGGCTTGAAGTTCAAAGTAGTTGAGTCTCTTTATTATTG | 2241 |
| M1.1.2 | AGGGAAGAAAGAGAGTGTGGCTTGAAGTTCAAAGTAGTTGAGTCTCTTTATTATTG | 2244 |
| Rp1-blb2 | AGGGAAGAAAGAGAGTGTGGCTTGAAGTTCAAAGTAGTTGAGTCTCTTTATTATTG | 2274 |
| | ***** * * * * * | ***** * * * * * |

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Figure 16 (cont.)

| | | |
|----------|--|------|
| M1.1.1 | ACAGCTGAAGTGGAAAGTGATGAAGTTATAGAAATTAAGTTATGACCACTTTACCACATCAC | 2301 |
| M1.1.2 | ACAGCTGAAGTGGAAAGTGATGAAGTTATAGAAATTAAGTTATGACCACTTTACCACATCAC | 2304 |
| Rp1-blb2 | ACAGATGAAGTGGAAAGTGATGAAGTTATAGAAATTAAGTTATGACCACTTTACCACATCAC | 2334 |
| | * * * * * | |
| M1.1.1 | CTCAAGCCATGCTTCGTGTAATTTTCGAAGTTTCCGAAGCACTTCATTGACAACTAT | 2361 |
| M1.1.2 | CTCAAGCCATGCTTCGTGTAATTTTCGAAGTTTCCGAAGCACTTCATTGACAACTAT | 2364 |
| Rp1-blb2 | CTCAAGCCATGCTTCGTGTAATTTTCGAAGTTTCCGAAGCACTTCATTGACAACTAT | 2394 |
| | * * * * * | |
| M1.1.1 | GAGTTGATGTTTATTTTCGGTCTGAGGATTTTGGGGAAGACGAGATGAACAGTATG | 2421 |
| M1.1.2 | TGTTTACTGTTTATTTGGGTGCTGAGGATTTTGGGGAAGACGAGATGAACAGGATTA | 2424 |
| Rp1-blb2 | GAGTTGAAACTTATTTGGGTTTTGAGGATTTTGGGGAAGACGAGATGAAGAGTCTG | 2454 |
| | * * * * * | |
| M1.1.1 | GAAGAAGTGGTGAAGATTTATATGGATGATTTAATTACAGTAGCTTGGTAATTTGTTTC | 2481 |
| M1.1.2 | GAAGAAGTGGTGAAGATTTATATGGATGATTTAATTCCAGTAGCTTGGTAATTTGTTTC | 2484 |
| Rp1-blb2 | GAGAAGTGGTGAAGATTTATTTGGATGATTTAATTCCAGTAGCTTGGTAATTTGTTTC | 2514 |
| | * * * * * | |
| M1.1.1 | AATGAGATPAGGTATGACATGAATTTCCAAATTCATGATCTTGTGCATGACTTTTGTG | 2541 |
| M1.1.2 | AATGAGATPAGGTATGACATGAATTTCCAAATTCATGATCTTGTGCATGACTTTTGTG | 2544 |
| Rp1-blb2 | AATGAGATPAGGTATGACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTAC | 2574 |
| | * * * * * | |
| M1.1.1 | ATAAAGCAAGAAAGGAAATTTGTTGATCAGATPAGATCAAGTGTCTCCATCAGATTG | 2601 |
| M1.1.2 | ATAAAGCAAGAAAGGAAATTTGTTGATCAGATPAGATCAAGTGTCTCCATCAGATTG | 2604 |
| Rp1-blb2 | ATAAAGCAAGAAAGGAAATTTGTTGATCAGATPAGATCAAGTGTCTCCATCAGATTG | 2634 |
| | * * * * * | |
| M1.1.1 | TTCCTGTGTCAAATPACCATTGATGTGATGAGGAGGAG---CACTTTGGGCTTAATTTT | 2658 |

Annotated Sheet Showing Changes

53/62**Figure 16 (cont.)**

| | | |
|----------|---|------|
| M1.1.2 | TTGCCGTGTCMAATTACCATTGATTATGATGAGGAGGAGGACACTTTGGGCTTAATTTT | 2664 |
| Rpl-b1b2 | TTGCCACGTCMAATTAGCATTTGATGATGATGAAGAGCCTTTGGGCTTAATTTT | 2694 |
| | ***** | |
| M1.1.1 | GTCAATGTCGATTCAAATAGAAAGAGGCATTCTGGTAAACACACTCTATCTTTGAGGATA | 2718 |
| M1.1.2 | GTCAATGTCGATTCAAATAGAAAGAGGCATTCTGGTAAACACCTCTATCTTTGAGGATA | 2724 |
| Rpl-b1b2 | GTCCGTGTCGGTTCAAATAGAAAGAGGCATTCCGGTAAACACCTCTATCTTTGAGCATA | 2754 |
| | *** | |
| M1.1.1 | ATTGGAGACAGCTGGATGACAGTGTTCCTGATGCATTTCCACTAAGACACTTGAGGCTT | 2778 |
| M1.1.2 | AATGGAGACAGCTGGATGACAGTGTTCCTGATGCATTTCCACTAAGACACTTGAGGCTT | 2784 |
| Rpl-b1b2 | AATGGAGATGAGCTGGAGCACCATTCTTCGTATGATTCATCTAAGACACTTGAGGCTT | 2814 |
| | * ***** | |
| M1.1.1 | CTTAGAGTGTGGACCTGCATACGCTCTTTTATCATGTGGTAAAGATCTTTTGCTGAATGAA | 2838 |
| M1.1.2 | ATTAGAGTGTGGACCTGCATACGCTCTTTTAAATCATGTGGTAAAGATCTTTTGCTGAATGAA | 2844 |
| Rpl-b1b2 | CTTAGAACCTTGCACCTGGAACTCCTTTTATCATGTGTTAAAGATCTTTTGCTGAATGAA | 2874 |
| | ***** | |
| M1.1.1 | ATATGCATGTTGGAATCATTTGAGGTACTTATCCATGACACACAAAGTTAAATATCTGCCT | 2898 |
| M1.1.2 | ATATGCATGTTGGAATCATTTGAGGTACTTAAAGATTCGGACACAAAGTTAAATATCTGCCT | 2904 |
| Rpl-b1b2 | ATATGCATGTTGGAATCATTTGAGGTACTTAAAGCATTTGGACACAAAGTTAAATCTCGCCT | 2934 |
| | ***** | |
| M1.1.1 | TTGCTTTTCTCAAACCTCTGGAATCTAGAAAGCTGTTTGTGTCTACACACAGATCAATC | 2958 |
| M1.1.2 | TTGCTTTTCTCAAACCTCTGGAATCTAGAAAGCTGTTTGTGTCTACAAAGGATCAATC | 2964 |
| Rpl-b1b2 | TGTCTTTTCTCAAACCTCTGGAATCTAGAAATCTTGTGTGTGATPACAAAGATCAAC | 2994 |
| | ** ***** | |
| M1.1.1 | TTGGTACTATTACCGAGAAATTTTGGATCTTGTTAAAGTTGCGAGTGTCTCCGTGGATGCT | 3018 |
| M1.1.2 | TTGGTACTATTATCCGAGAAATTTTGGATCTTGTAAAGTTGCGAGTGTCTCCGTGGATGCT | 3024 |

Figure 16 (cont.)

| | | |
|----------|--|------|
| Rpl-b1b2 | TTGATACATATTACCGAGAAATTTGGGATCTGTGTAAGTTGCAAGTCTGTTCACAGCTGCT | 3054 |
| | *** ***** | |
| M1.1.1 | TGTTCTTCTTTGATATGATGTCAGATCATANTATGATAGCAGGGACACAAAGTTA | 3078 |
| M1.1.2 | TGTTCTTCTTTGATATGATGTCAGATGATCAATATGATAGCAGGGACACAAAGTTA | 3084 |
| Rpl-b1b2 | TGTTCTTCTTTGATATGATGTCAGATGATCAATACTGATAGCAGGGACACAAAGTTA | 3114 |
| | ***** | |
| M1.1.1 | GAGAATTTGAGAATATTACGGGAATGTTGATTTCTTATTCGAAAGATACAAAGAAATTT | 3138 |
| M1.1.2 | GAGAATTTGAGAATATTAGGGGAATGTTGATTTCTTATTCGAAAGATACAAAGAAATTT | 3144 |
| Rpl-b1b2 | GAGAATTTGACAGCATTAGGGGAATGCTGTTCTTATTCGAAAGATACAGAGGATTT | 3174 |
| | ***** | |
| M1.1.1 | TTCAAAGGTTTCCCAATCTTCAGTTCCTTCATTTGAACCTCAGGAGTCATGGGATAT | 3198 |
| M1.1.2 | TTCAAAGGTTTCCCAATCTTCAGTTCCTTCAGTTCCTTCATTTGAACCTCAGGAGTCATGGGATAT | 3204 |
| Rpl-b1b2 | TTCAAAGGTTTCCCAATCTTCAGTTCCTTCATTTGAACCTCAGGAGTCATGGGATAT | 3234 |
| | ***** | |
| M1.1.1 | TCACAGAGCAACATTTGGTTCGGAATTTGGATTTTCCTTACCTGAACTAGAAACACTCTCT | 3258 |
| M1.1.2 | TCACAGAGCAACATTTGGTTCGGAATTTGGATTTTCCTTACCTGAACTAGAAACACTCTGT | 3264 |
| Rpl-b1b2 | TCACAGAGCAACATTTGGTTCGGAATTTGGATTTTCCTTACCTGAACTAGAAACACTCACT | 3294 |
| | ***** | |
| M1.1.1 | GTAGGTTTTAAAGTTCAAAACAAACGATAGTGGGTCTCTGTAGCGCAAAATCGGCGC | 3318 |
| M1.1.2 | GTAGGTTTTAAAGTTCAAAACAAACGATAGTGGGTCTCTGTGTGACAAATCGGCGC | 3324 |
| Rpl-b1b2 | GTAGGTTTTGAAGATCAAAACAAATGACATGGGTCTCTGTGACGCCAATAATCGGCCA | 3354 |
| | ***** | |
| M1.1.1 | TGGATTTTCACTTCCCTCAAAATTGAAAATACGTGTGGTGCCTGAAATTCGCGTGACA | 3378 |
| M1.1.2 | TGGATTTTCACTTCCCTCAAAATTGAAAAGACTGTGTGTATGACTTTCTCTGACA | 3384 |
| Rpl-b1b2 | TGGATTTTCACTTCCCTCGAGTTTGAAGAATTGCAATTCATGAAATTTCTCTGACA | 3414 |

Figure 16 (cont.)

| | | |
|----------|------------------------------|------|
| Mil.1 | GGCCAAAGAATATCCCTTATTTAAGTAG | 3768 |
| Mil.2 | GGCCAGAAGATATCCCTTATTTAAGTAG | 3774 |
| Rp1-b1b2 | GGCCAGAAGATATCCCGTATTTAAGTAG | 3804 |
| | ***** | |

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Figure 17: Multiple Sequence Alignments of M1.1, M1.2 and Rpi-blb2 proteins

CLUSTAL W (1.82) Multiple Sequence Alignments

```

Sequence format is Pearson
Sequence 1: M1.1 1255 aa
Sequence 2: M1.2 1257 aa
Sequence 3: Rpi-blb2 1267 aa
Start of Pairwise Alignments
Aligning...
Sequences (1:2) Aligned. Score: 91
Sequences (1:3) Aligned. Score: 82
Sequences (2:3) Aligned. Score: 81
Guide tree file created: [/ebi/extern/clusterw-work/interactive/clusterw-20040503-14322840.dnc,
Start of Multiple Alignment
There are 2 groups
Aligning...
Group 1: Sequences: 2 Score:25939
Group 2: Sequences: 3 Score:24668
Alignment Score 19405
CLUSTAL-Alignment file created [/ebi/extern/clusterw-work/interactive/clusterw-20040503-14322840.aln]

```

CLUSTAL W (1.82) multiple sequence alignment

M1.1 MEKKNEEANNLIVLSALSKDIADVLFLE--NEENQALDKDQVEKIKLQWAFICT 57

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Figure 17 (cont.)

| | | | |
|----------|-----------------------------------|-------------------------------|-----|
| M1.1.2 | MEKRKIDEEANNSLVFSALSQDIANVLFLE--- | NEENOKALDKQVEKLLKQWAFICT | 57 |
| Rp1-blb2 | MEKRKIDEEANNSLVFSALSQDIANVLFLE--- | LKNEEDQKAVDVLIESLKLKTICT | 60 |
| | ***** | ***** | |
| M1.1.1 | YVQLSGSDFEQFEDIMTRKRQEVENLLQPLD | DDDD-----VFTSLTSNMDDCISLYHR | 109 |
| M1.1.2 | YVQLSYSDFEQFEDIMTRKRQEVENLLQSLD | DDDD-----VFTSLTSNMDDCISLYHR | 109 |
| Rp1-blb2 | YVQLSYSDLEKFEDIMTRKRQEVENLLQPLD | DDDDGKDVCGKVLTSLAGNMDDCISLYHR | 120 |
| | ***** | ***** | |
| M1.1.1 | SYKSDAIMMDEQDLFLLNLVHLSKHA | EKIFPGVTQYEVQLQNGNIRD | 169 |
| M1.1.2 | SYKSDAIMMDEQDLFLLNLVHLSKHA | EKIFPGVTQYEVQLQNGNIRD | 169 |
| Rp1-blb2 | S-KSDATMDEQLGFLLLNLVHLSKHA | EKIFPGVTQYEVQLQNGNIRD | 179 |
| | ***** | ***** | |
| M1.1.1 | KHEMVENVLPFLQMA | DRVGHFLMDQDDEDSRLSELDEQND | 229 |
| M1.1.2 | KHEMVENVLPFLQMA | DRVGHFLMDQDDEDSRLSELDEQND | 229 |
| Rp1-blb2 | KHEMVENVLSLQMA | ERVGHFLMDQDDEDSRLSELDEQND | 239 |
| | ***** | ***** | |
| M1.1.1 | PVELEVVIHCYTNL | KASTSAEVGFLFKQLLETSPDILREYLI | 289 |
| M1.1.2 | PTELEVMIHCYTNL | KASTSAEVGRFINKLLETSPDILREYLI | 289 |
| Rp1-blb2 | PTELEVMIHCYTK | KASTSTGIRFKLLETSPDILREYLI | 299 |
| | ***** | ***** | |
| M1.1.1 | NIHVMMFELLIL | LSDM-P-KDFIHHDKLPDL | 348 |
| M1.1.2 | NIHVMMFELLIL | LSDM-P-KDFIHHDKLPDL | 348 |
| Rp1-blb2 | NIHVMMFELLIL | SDMPNDPFIHHDKLPDL | 359 |
| | ***** | ***** | |
| M1.1.1 | TNCATDILLENIELL | KOLKHVYLKALDSQCCPFMSD | 408 |
| M1.1.2 | TNCATDILLENIELL | KOLKHVYLKALDSQCCPFMSD | 408 |

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Figure 17 (cont.)

| | |
|----------|--|
| Rp1-blb2 | TNCATCTFLENIELLKEDLKHVYIKVDPSSOYCFPMSSDGLFPHLLQRLHLDLDDLSNAYS 419 *****:*****:*****:*** *****:***:***** |
| M1.1 | IALIKEIEIYVKODLFTFRSEFVD-AEQGLYKDWARVLVDVAYEAKDVIDSIIVRDNGLL 467 |
| M1.2 | ISLIEIEIYVSEIEIETFRSFGDAEEQGLYKDWARVLVDVAYEAKDVIDSIIVRDNGLL 468 |
| Rp1-blb2 | IALIKEQIGLVKEDLFTFRSFFAN-TEQGLYKDWERVLVDVAYEAKDVIDSIIVRDNGLL 478 *:*:*:* *:::*****: *****:* *****:***** |
| M1.1 | HLIFSIPITIKIKLKEIEISALDENI PKDRGLIVNSPKKEVERKSLTTDKITVGFEE 527 |
| M1.2 | HLIFSIPITIKIKLKEIEISALDENI PKDRGLIVNSPKKEVERKSLTTDKIIVGFEE 528 |
| Rp1-blb2 | HLIFSIPITRKQMLIKKEEVDLHENI SKNRGLIVNSPKKEVERKSLTTDKIIVGFEE 538 ***** ** : *****: *.*.*:***** ***** ***** ** * |
| M1.1 | TNLIIRKLTSGADLDVLSITGMPSGSKTTLAYKVYNDKSVSSRFDLRACVTDQGCDEK 587 |
| M1.2 | TNLIIRKLTSGADLDVLSITGMPSGSKTTLAYKVYNDKSVSSRFDLRACVTDQGDIDK 588 |
| Rp1-blb2 | TNLIIRKLTSGADLDVLSITGMPSGSKTTLAYKVYNDKSVSSRFDLRACVTDQGVYDEK 598 *****:***** ***** ***** ***** ***** ***** *:* |
| M1.1 | KLINTIFSOVSDSKLSLENIDVADKLKQLFGKRYLIVLDDVMDTTTWDLTTRPFPPEK 647 |
| M1.2 | KLIDTIFSOVSGSDSLSENIDVADKLKQLFGKRYLIVLDDVMDTTTLDLTTRPFPPEK 648 |
| Rp1-blb2 | KLIDKIFNQVSGSDSLSENIDVADKLKQLFGKRYLIVLDDVMDTTTWDLTTRPFPPEK 658 *:*:*.*.*:***** ***** ***** ***** * *****:* |
| M1.1 | KGSRIILTTRKEVALHGKLTDPDLRLRPDESWELEKRAFENSCPDELLDVGKEI 707 |
| M1.2 | KGSRIILTTRKEVALHGKLTDPDLRLRPDESWELEKRTFENSCPDELLDVGKEI 708 |
| Rp1-blb2 | KGSRIILTTRKEVALHGKLTDPDLRLRLRSEESWELEKRAFENSCPDELLDVGKEI 718 *****:***** *****:*****:*****:*****:***** |
| M1.1 | AENCKGLPLVADLIAGTAGREKKRSVWLEQSSLSFINSSEVEMKVIETSYDHLPHH 767 |
| M1.2 | AENCKGLPLVADLIAGTAGREKKRSVWLEQSSLSFINSSEVEMKVIETSYDHLPHH 768 |
| Rp1-blb2 | AENCKGLPLVVDLIAGTAGREKKRSVWLEVVNNLHFSFLKNEVEVMKVIETSYDHLPDH 778 |

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Figure 17 (cont.)

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M11.1      SDSLSTIARLNFLELSLYHTIIHGEWNMGEDTFENLKFNFNOVSIKWEVGEESFP 1186
M11.2      SDSLSTIARLNFLENSLYDTIIQGEWNMGEDTFENLKFNLRLITLSKWEVGEESFP 1188
Rp1-blb2   SDSLSTIARLNFLEELIYIRTIHGEWNMGEDTFENLKCMLSQVILTSKWEVGEESFP 1190
          ***** * : *****
          ***** * : *****

M11.1      NLEKLRGCHKLEIIPPSFGDIYSLKSIKIVKSPQLEDSALKIKYAEADMGGDELQIL 1246
M11.2      NLEKLRQECGLEIIPPSFGDIYSLKFIVKSPQLEDSALKIKYAEADMGGNDLQIL 1248
Rp1-blb2   TLEKLESDCHNLEIIPPSFGDIYSLKLEIIVRSPQLENSALKIKYAEADMGGDELQIL 1258
          ***** * : *****
          ***** * : *****

GQNIPLFK 1255
GQNIPLFK 1257
GQDIPLFK 1267
          *****
```

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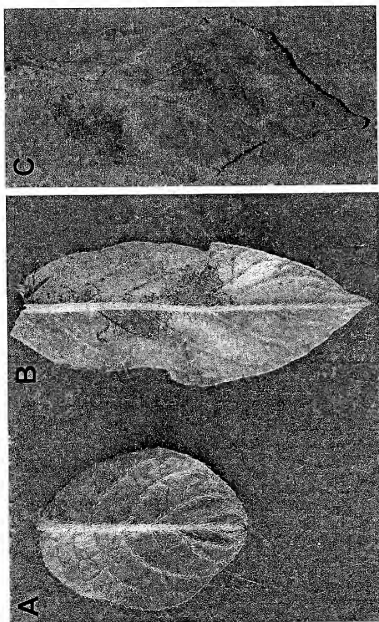


Figure 18